

Amendments to the Claims:

The following listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Previously Presented) A method for assaying the presence or the absence of at least one mutation on a strand of nucleic acids paired in a duplex form, comprising:
 - contacting in a liquid medium said duplex, suspected to include at least one mismatch with at least one compound able to undergo a specific base pairing interaction with said mismatch, said compound(s) being used at a combined concentration of at least 10g/l in said medium; and
 - assaying for said mismatch by an analytical method.
2. (Original) The method according to claim 1, wherein the strands of nucleic acids paired in duplex form are two DNA strands which are in all or in part complementary.
3. (Currently Amended) A method for performing Electrophoretic Heteroduplex Analysis "EHDA" on a nucleic acid sample suspected to include at least one heteroduplex, comprising:
 - contacting in a liquid medium said nucleic acid sample suspected to include at least one heteroduplex, with at least one compound able to undergo a specific base pairing interaction with at least one mismatch of said heteroduplex, said compound(s) being used at a combined concentration of at least 10g/l of said medium,
 - assaying for the presence of said heteroduplex ~~thanks to~~based on its electrophoretic mobility.
4. (Currently Amended) The method according to claim 3 comprising a preliminary step of denaturating the nucleic acid sample and renaturating it ~~in~~under conditions ~~convenient to~~that achieve both heteroduplexes and homoduplexes.

5. (Previously Presented) A method for assaying the presence or the absence of at least one mutation on a single strand of nucleic acid in a liquid medium, comprising:

- (a) contacting said nucleic acid suspected to include at least one mutation with a nucleic acid probe grafted on a solid support,
- (b) allowing the hybridization of at least a part of said strand of nucleic acid with the grafted nucleic acid probe,
- (c) washing non-hybridized strands, and
- (d) assaying for said mutation by an analytical method,

wherein the steps a) and/or c) are performed in the presence of at least one compound able to undergo a specific base pairing interaction with said mutation, said compound being at a concentration of at least 1g/l.

6. (Previously Presented) The method according to claim 1 wherein the strand(s) of nucleic acids is a single stranded DNA, RNA, LNA, PNA, or any artificial or natural analog of nucleic acids.

7. (Currently Amended) The method according to claim 1, wherein the compound able to undergo a specific base pairing interaction includes at least two groups suitable for hydrogen bonding, in an orientation, polarity and spacing compatible with the creation of attractive interaction with at least one of the bases A, T, G, C, and U.

8. (Previously Presented) The method according to claim 1, wherein said compound is unable to interfere with polymerisation reactions of nucleotides and/or to be incorporated into a newly polymerized DNA strand.

9. (Currently Amended) The method according to claim 1, wherein said compound is ~~one oligonucleotide having a length of less than 5 nucleotides, a nucleoside, a base or a mixture thereof selected from the group consisting of oligonucleotides less than 5 nucleotides in length, nucleosides, bases, and mixtures thereof.~~

10. (Currently Amended) The method according to claim 9, wherein the oligonucleotide has a length of oligonucleotides are less than 3 nucleotides in length.

11. (Currently Amended) The method according to claim 9, wherein the compound is selected among from the group consisting of adenosine, guanosine, uridine, cytidine, thymidine, and mixtures thereof.

12. (Currently Amended) The method according to claim 9, wherein oligonucleotide(s) or nucleoside(s) in the mixture of oligonucleotides or nucleosides are unable to undergo mutually base pairing interaction the oligonucleotides less than 5 nucleotides in length, the nucleosides, the bases, and the mixture thereof are unable to undergo base pairing interactions with each other.

13. (Currently Amended) The method according to claim 12, wherein the compound includes cytidine and thymidine, or cytidine and adenosine, or guanosine and thymidine, or guanosine and adenosine.

14. (Previously Presented) The method according to claim 1, wherein the compound(s) is used at a concentration of at least 25 g/l.

15. (Currently Amended) The method according to claim 1, in which wherein said compound(s) is in addition bearing has at least one substituent.

16. (Currently Amended) The method according to claim 15, in which wherein said substituent induces in said compound at least one of the following changes change selected from the group consisting of:

an increase in solubility,

a change in charge, or and

a change in friction with a solvent.

17. (Currently Amended) The method according to claim 1, wherein the mutation ~~to assay~~ is a point mutation.

18. (Currently Amended) The method according to claim 1, wherein said mutation is assayed by a hybridization assay.

19. (Previously Presented) The method according to claim 1, wherein said mutation is assayed by an electrophoretic analysis using a liquid separating medium.

20. (Previously Presented) The method according to claim 19, wherein said liquid separating medium contains at least a polymer at a concentration of at least 1% by weight of the total weight of said medium.

21. (Currently Amended) The method according to claim 19, wherein said liquid separating medium contains at least ~~a~~one polymer ~~chosen~~selected from the group consisting of N,N-disubstituted polyacrylamides and N- substituted polyacrylamides, wherein said N substituents are selected from the group consisting of C₁ to C₁₂ ~~alkyl, alkyls~~, halo-substituted C₁ to C₁₂ ~~alkyl, alkyls~~, methoxy-substituted C₁ to C₁₂ ~~alkyl, alkyls~~, and hydroxyl-substituted C₁ to C₁₂~~alkyl alkyls~~.

22. (Currently Amended) The method according to claim 20, wherein the liquid separation medium contains at least one polymer composed of several polymer segments, said polymer being of ~~the~~an irregular block copolymer type or irregular comb polymer type and having on average at least three junction points established between polymer segments of different chemical or topological nature.

23. (Previously Presented) The method according to claim 22, wherein the polymer comprises at least one type of polymer segment showing, within the separating medium, specific affinity for a channel wall, and at least one type of polymer segment showing in said medium less or no affinity for said wall.

24. (Previously Presented) The method according to claim 20, wherein said polymer contains acrylamide or substituted acrylamides.

25. (Currently Amended) A method for diagnosing a predisposition to genetic diseases or cancers used in determining whether a patient is predisposed to a cancer or a genetic disease known to be associated or putatively associated to with a specific point mutation(s)-mutation, or used in diagnosing a patient suspected of suffering from said cancer or disease, or used in determining a prognosis of a patient diagnosed as having said cancer or disease, the diagnosis or prognosis of said diseases or cancers, the method comprising:

obtaining from the patient a nucleic acid suspected to include at least one mismatch corresponding to the specific point mutation;

contacting placing the nucleic acid, paired in duplex form, in a liquid medium and contacting the nucleic acid-said duplex, suspected to include at least one mismatch with at least one compound able to undergo a specific base pairing interaction with said mismatch, said compound(s)-at least one compound being used at a combined concentration of at least 10g/l in said medium; and

assaying for said mismatch by an analytical method to detect whether said mismatch is present, wherein the presence of said mismatch indicates that the nucleic acid has the specific point mutation known to be associated or putatively associated with the cancer or the genetic disease.

26. (Currently Amended) The method according to claim 25, wherein said disease is associated to at least a point mutation is in a human breast cancer predisposition gene (BRCA).

27. (Currently Amended) A composition including at least comprising a compound able to undergo specific base pairing interaction at a concentration of at least 1 g/l and at least being present in a liquid separating medium that comprises at least one polymer at a concentration of at least 1% by weight.

28. (Currently Amended) The composition according to claim 27, wherein the compound able to undergo a specific base pairing interaction includes at least two groups suitable for hydrogen bonding, in an orientation, polarity and spacing compatible with ~~the-a~~ creation of attractive interaction with at least one of ~~the-bases~~ A, T, G, ~~C-C~~, and U.

29. (Canceled)

30. (Currently Amended) The composition according to claim 27, wherein said liquid separation medium ~~includes furthermore at least a compound~~ comprises one member selected ~~among~~ from the group consisting of:

~~a-sieving polymer polymers,~~

~~a-hydrophilic polymer, polymers, and~~

~~a-surface-active polymer polymers.~~

31. (Currently Amended) A composition ~~including at least comprising~~ a DNA fragment having a nucleic sequence related to a gene on which a point mutation(s) has been associated or putatively associated with a disease or an increased predisposition to a disease, and ~~at least~~ a compound able to undergo specific base pairing ~~interaction, said compound(s)~~ being used ~~interaction~~ at a concentration of at least 10g/l, wherein said compound able to undergo a specific base pairing interaction includes at least two groups suitable for hydrogen bonding, in an orientation, polarity and spacing compatible with ~~the-a~~ creation of attractive interaction with at least one of ~~the-bases~~ A, T, G, ~~C-C~~, and U.

32. (Currently Amended) A composition ~~including at least comprising~~ a compound able to undergo specific base pairing interaction at a concentration of at least 1g/l, 10 g/l, and a pair of DNA probes, wherein said compound able to undergo a specific base pairing interaction includes at least two groups suitable for hydrogen bonding, in an orientation, polarity and spacing compatible with ~~the-a~~ creation of attractive interaction with at least one of ~~the-bases~~ A, T, G, ~~C-C~~, and U.

33. (Currently Amended) A kit useful for the screening of a nucleic acid ~~or analog~~
~~thereof and/or nucleic acid analogs~~ having a sequence related to a gene on which point
mutation(s) has been associated or putatively associated with a disease or an increased
predisposition to a disease, said kit comprising at least ~~a~~one composition according to claim
27.

34. (Currently Amended) A method for assaying a nucleic acid for mutation,
comprising:

performing a polymerase chain reaction on said nucleic acid in the presence of
at least two primers and a pool of compounds able to undergo specific base pairing interaction
with nucleotides ~~or analogue thereof, and/or nucleotide analogues~~, said compounds being at a
combined concentration of at least ~~1-4~~10 g/l and being unable to interfere with the
polymerase chain reaction; and

analyzing and/or quantifying the so-obtained DNA fragments.

35. (Currently Amended) The method according to claim 34, wherein the
compound able to undergo a specific base pairing interaction includes at least two groups
suitable for hydrogen bonding, in an orientation, polarity and spacing compatible with ~~the~~a
creation of attractive interaction with at least one of ~~the~~the bases A, T, G, C, and U.

36. (New) The method according to claim 25, wherein the method is used in
determining whether a patient is predisposed to a cancer or a genetic disease known to be
associated or putatively associated with a specific point mutation.

37. (New) A method for assaying for the presence of a mismatch on a nucleic acid
in duplex form, the method comprising:

contacting the nucleic acid with a composition comprising a compound able to
undergo specific base pairing interaction at a concentration of at least 1 g/l present in a liquid
separating medium; and

assaying for a mismatch in the nucleic acid to detect whether the mismatch is present.

38. (New) A method for assaying for the presence of a mismatch on a nucleic acid in duplex form, the method comprising:

contacting a nucleic acid with a compound able to undergo specific base pairing interaction at a concentration of at least 10g/l; and
assaying for a mismatch in the nucleic acid to detect whether the mismatch is present;

wherein:

the nucleic acid comprises a nucleic sequence corresponding to a gene on which a point mutation is known to be associated with a disease or a predisposition to a disease; and

the compound able to undergo a specific base pairing interaction comprises at least two groups suitable for hydrogen bonding, in an orientation, polarity, and spacing compatible with a creation of attractive interaction with at least one of bases A, T, G, C, and U.

39. (New) A method for assaying for the presence of a mismatch on a nucleic acid in duplex form, the method comprising:

contacting the nucleic acid with a composition comprising a compound able to undergo specific base pairing interaction at a concentration of at least 10 g/l and a pair of DNA probes; and

assaying for a mismatch in the nucleic acid to detect whether the mismatch is present;

wherein:

the compound able to undergo a specific base pairing interaction comprises at least two groups suitable for hydrogen bonding, in an orientation, polarity, and spacing compatible with a creation of attractive interaction with at least one of bases A, T, G, C, and U.